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OM protein - protein search, using sw model

Run on: October 28, 2003, 08:57:32 ; Search time 28 Seconds
(without alignments)
10.578 Million cell updates/sec

Title: US-09-847-940B-6
Perfect score: 7
Sequence: 1 XXXXXXX 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	7	100.0	7	1	US-07-700-526-17
2	7	100.0	7	1	US-07-690-284A-8
3	7	100.0	7	1	US-07-690-284A-12
4	7	100.0	7	1	US-07-720-222-21
5	7	100.0	7	1	US-07-855-793-2
6	7	100.0	7	1	US-07-866-678-2
7	7	100.0	7	1	US-07-866-678-6
8	7	100.0	7	1	US-07-866-678-10
9	7	100.0	7	1	US-07-670-296-5
10	7	100.0	7	1	US-07-670-296-12
11	7	100.0	7	1	US-07-689-693B-17
12	7	100.0	7	1	US-07-712-838B-7
13	7	100.0	7	1	US-07-663-413-20
14	7	100.0	7	1	US-07-663-413-25
15	7	100.0	7	1	US-07-596-867C-8
16	7	100.0	7	1	US-07-657-769B-11
17	7	100.0	7	1	US-07-657-769B-51
18	7	100.0	7	1	US-07-935-310A-4
19	7	100.0	7	1	US-07-778-233B-25
20	7	100.0	7	1	US-07-718-274A-26
21	7	100.0	7	1	US-07-718-274A-28
22	7	100.0	7	1	US-07-718-274A-51
23	7	100.0	7	1	US-07-718-274A-63
24	7	100.0	7	1	US-07-715-650-2
25	7	100.0	7	1	US-07-830-330-5
26	7	100.0	7	1	US-07-626-923A-7
27	7	100.0	7	1	US-07-883-491-1

28	7	100.0	7	1	US-07-715-183C-14	Sequence 14, Appl
29	7	100.0	7	1	US-07-748-292-10	Sequence 10, Appl
30	7	100.0	7	1	US-07-946-234A-5	Sequence 5, Appl
31	7	100.0	7	1	US-07-893-930-34	Sequence 34, Appl
32	7	100.0	7	1	US-07-789-344A-13	Sequence 13, Appl
33	7	100.0	7	1	US-08-044-547-10	Sequence 10, Appl
34	7	100.0	7	1	US-07-989-962-8	Sequence 8, Appl
35	7	100.0	7	1	US-07-989-962-11	Sequence 11, Appl
36	7	100.0	7	1	US-07-989-962-12	Sequence 12, Appl
37	7	100.0	7	1	US-07-989-962-13	Sequence 13, Appl
38	7	100.0	7	1	US-07-989-962-14	Sequence 14, Appl
39	7	100.0	7	1	US-07-989-962-15	Sequence 15, Appl
40	7	100.0	7	1	US-07-989-962-16	Sequence 16, Appl
41	7	100.0	7	1	US-07-989-962-17	Sequence 17, Appl
42	7	100.0	7	1	US-07-989-962-20	Sequence 20, Appl
43	7	100.0	7	1	US-07-989-962-21	Sequence 21, Appl
44	7	100.0	7	1	US-07-989-962-22	Sequence 22, Appl
45	7	100.0	7	1	US-07-989-962-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-07-700-526-17
; Sequence 17, Application US/07700526
; Patent No. 5166133
; GENERAL INFORMATION:
; APPLICANT: Houston, L. L.
; APPLICANT: Liu, David Y.
; APPLICANT: Kaymakalan, Zehra
; TITLE OF INVENTION: Method for Inhibiting Adhesion of White
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/700,526
; FILING DATE: 19910816
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 2600.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3217
; TELEFAX: (415) 658-5239
; TELEX: 4992659
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-700-526-17

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
; : : : : : :

/ MOLECULE TYPE: peptide
US-07-720-222-21
Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XXXXXX 7
Db 1 SRRGMS 7
RESULT 5
US-07-855-793-2
; Sequence 2, Application US/07855793
; Patent No. 5217880
; GENERAL INFORMATION:
; APPLICANT: Masanori MITTA et al.
; TITLE OF INVENTION: L-FUCOSE DEHYDROGENASE GENE,
; TITLE OF INVENTION: MICROORGANISM HAVING SAID GENE AND PRODUCTION OF L-FUCOSE
; TITLE OF INVENTION: DEHYDROGENASE BY THE USE OF SAID MICROORGANISM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/855,793
; FILING DATE: 19920323
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE: internal fragment
; ORIGINAL SOURCE:
; ORGANISM: Arthrobacter Oxidans
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:

/ CHROMOSOME/SEGMENT:
/ MAP POSITION:
/ UNITS:
/ FEATURE:
/ NAME/KEY:
/ LOCATION:
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION:
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ TITLE:
/ JOURNAL:
/ VOLUME:
/ ISSUE:
/ PAGES:
/ DATE:
/ DOCUMENT NUMBER:
/ FILING DATE:
/ PUBLICATION DATE:
/ RELEVANT RESIDUES IN SEQ ID NO:
US-07-855-793-2
Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XXXXXX 7
Db 1 WGAGMNQ 7
RESULT 6
US-07-866-678-2
; Sequence 2, Application US/07866678
; Patent No. 522531
; GENERAL INFORMATION:
; APPLICANT: Gresham, Hattie D.
; APPLICANT: Brown, Eric J.
; APPLICANT: Adams, Steven P.
; TITLE OF INVENTION: No. 5225531el Hexapeptide
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/866,678
; FILING DATE: 19920409
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24 (867) A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-866-678-2
Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 AKQAGDV 7

RESULT 7

US-07-866-678-6
; Sequence 6, Application US/078666678
; Patent No. 5225531
; GENERAL INFORMATION:
; APPLICANT: Gresham, Hattie D.
; APPLICANT: Brown, Eric J.
; APPLICANT: Adams, Steven P.
; TITLE OF INVENTION: No. 5225531el Hexapeptide
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866,678
FILING DATE: 19920409
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24 (867)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-866-678-6

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 KGALEVA 7

RESULT 8

US-07-866-678-10
; Sequence 10, Application US/078666678
; Patent No. 5225531
; GENERAL INFORMATION:
; APPLICANT: Gresham, Hattie D.
; APPLICANT: Brown, Eric J.
; APPLICANT: Adams, Steven P.
; TITLE OF INVENTION: No. 5225531el Hexapeptide
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866,678
FILING DATE: 19920409
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24 (867)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-866-678-10

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 GRGDSPA 7

RESULT 9

US-07-670-296-5
; Sequence 5, Application US/07670296
; Patent No. 5229364

GENERAL INFORMATION:

APPLICANT: Chiodi, Francesca

TITLE OF INVENTION: POLYPEPTIDES DERIVED FROM THE HUMAN

TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS ENDONUCLEASE PROTEIN

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Shore, Suker & Milnamow

STREET: 11300 Sorrento Valley Road, Suite 200

CITY: San Diego

STATE: CA

COUNTRY: U.S.A.

ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/670,296

FILING DATE: 19910607

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Bingham, Douglas A.

REGISTRATION NUMBER: 32,457

REFERENCE/DOCKET NUMBER: BCI-0009P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-1555

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: N-terminal

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FEATURE:
NAME/KEY: Region
LOCATION: 1..7
OTHER INFORMATION: /note= "An amino terminal group
OTHER INFORMATION: representing amino acid residue "Xaa" at position
OTHER INFORMATION: #1, in Sequence I.D. #1."
US-07-670-296-5

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
Db 1 GYIEAEV 7

RESULT 10
US-07-670-296-12
; Sequence 12, Application US/07670296
; Patent No. 5229364
; GENERAL INFORMATION:
; APPLICANT: Chiodi, Francesca
; TITLE OF INVENTION: POLYPEPTIDES DERIVED FROM THE HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS ENDONUCLEASE PROTEIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & Milnamow
; STREET: 11300 Sorrento Valley Road, Suite 200
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/670,296
; FILING DATE: 19910607
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bingham, Douglas A.
; REGISTRATION NUMBER: 32,457
; REFERENCE/DOCKET NUMBER: BCI-0009P
; TELEPHONE: 619-546-1555
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..7
; OTHER INFORMATION: /note= "A carboxy terminal group
; OTHER INFORMATION: representing amino acid residue "Xaa" at position
; OTHER INFORMATION: #22, in Sequence I.D. #1."
US-07-670-296-12

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
Db 1 TIHTDNG 7
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RESULT 11
US-07-689-693B-17
; Sequence 17, Application US/07689693B
; Patent No. 5231011
; GENERAL INFORMATION:
; APPLICANT: David Hillyard
; APPLICANT: Baldomero M. Olivera
; TITLE OF INVENTION: Segregated Folding Determinants
; TITLE OF INVENTION: for Small Disulfide-Rich Peptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5231011th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: Compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/689,693B
; FILING DATE: 19910418
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: na
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: 9925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: amino acid sequence from King Kong KKO
; NAME/KEY: conotoxin
; IDENTIFICATION METHOD: sequencer
US-07-689-693B-17

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
Db 1 DQNCDDG 7

RESULT 12
US-07-712-828B-7
; Sequence 7, Application US/07712828B
; Patent No. 5235039
; GENERAL INFORMATION:
; APPLICANT: Heath et al.
; TITLE OF INVENTION: Assay Method for Hydrolytic
; TITLE OF INVENTION: Enzymes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN.
```

QY COUNTRY: U.S.A.
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/712,828B
FILING DATE: 19010610
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-712-828B-7

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1, XXXXXX 7
Db 1 FFGLMGK 7

RESULT 13
US-07-663-413-20
; Sequence 20, Application US/07663413
; Patent No. 5240703
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED
; PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/663,413
FILING DATE: 19910301
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-663-413-20

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 LLSDKLG 7
RESULT 14
US-07-663-413-25
; Sequence 25, Application US/07663413
; Patent No. 5240703
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: ATTENUATED, GENETICALLY-ENGINEERED
; PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/663,413
FILING DATE: 19910301
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-663-413-25

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 MKWATWI 7

RESULT 15
US-07-596-867C-8
; Sequence 8, Application US/07596867C
; Patent No. 5244796
; GENERAL INFORMATION:
; APPLICANT: Levy, H. Richard
; APPLICANT: Lee, W. Theodore
; TITLE OF INVENTION: CLONED LEUCONOSTOC MESENTEROIDES GLUCOSE-6-
; PHOSPHATE DEHYDROGENASE GENES AND METHOD OF MAKING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wall and Roehrig
; STREET: 217 Montgomery Street
; CITY: Syracuse
; STATE: New York
; COUNTRY: United States of America
; ZIP: 13202
COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch Diskette, 360Kb storage
COMPUTER: IBM Compatible PC
OPERATING SYSTEM: MSDOS
SOFTWARE: Word Perfect, Ver. 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/596,867C
FILING DATE: 19901012
CLASSIFICATION: 435
PRIOR APPLICATION DATA: No. 5244796e
ATTORNEY/AGENT INFORMATION:
NAME: Bickel, Arthur S.
REGISTRATION NUMBER: 34123
REFERENCE/DOCKET NUMBER: 270 P 030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (315) 422 7383
TELEFAX: (315) 422 9331
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7
TYPE: AMINO ACID
STRANDEDNESS: No. 5244796 applicable
TOPOLOGY: Linear
MOLECULE TYPE: amino acid
HYPOTHETICAL: no
ANTI-SENSE: No. 5244796 applicable
FRAGMENT TYPE: internal
ORIGINAL SOURCE: Leuconostoc mesenteroides glucose 6-phosphate
ORIGINAL SOURCE: dehydrogenase
IMMEDIATE SOURCE: No. 5244796 applicable
POSITION IN GENOME: No. 5244796 applicable
PUBLICATION INFORMATION: No. 5244796e
US-07-596-867C-8

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 ENDFENA 7

Search completed: October 28, 2003, 09:02:30
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 08:57:32 ; Search time 39 Seconds
(without alignments)
17.261 Million cell updates/sec

Title: US-09-847-940B-6

Perfect score: 7

Sequence: 1 XXXXXX 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	7	100.0	7	1 XEYDGD	galactose oxidase
2	7	100.0	7	1 NYPG7	hypothalamic hepta
3	7	100.0	7	1 A61324	dermorphin - Rohde
4	7	100.0	7	2 A60139	fatty-acid synthas
5	7	100.0	7	2 S71867	glutathione transf
6	7	100.0	7	2 S71870	glutathione transf
7	7	100.0	7	2 JN0859	peptidyl-di-peptida
8	7	100.0	7	2 A60224	Met-enkephalin-Arg
9	7	100.0	7	2 S36662	dermorphin (lys-7)
10	7	100.0	7	2 S21230	dermorphin (trp-4,
11	7	100.0	7	2 PH1408	Ig heavy chain V r
12	7	100.0	7	2 S19630	ribosomal protein
13	7	100.0	7	2 S16364	opacity protein P.
14	7	100.0	7	2 S16365	opacity protein P.
15	7	100.0	7	2 A58512	venom heptapeptide
16	7	100.0	7	2 S08606	hypothetical prote
17	7	100.0	7	2 ECMUCR	catch-relaxing pep
18	7	100.0	7	2 A61081	tryptophyllin, bas
19	7	100.0	7	2 PQ0663	membrane protein -
20	7	100.0	7	2 B35890	RNA-directed DNA p
21	7	100.0	7	2 S20446	elastase - Pseudom
22	7	100.0	7	2 S57274	triacylglycerol li
23	7	100.0	7	2 A15398	choline oxidase (E
24	7	100.0	7	2 S09652	hypothetical prote
25	7	100.0	7	2 S55548	mcrB protein - Esc
26	7	100.0	7	2 S45311	microcin C7 - Esc
27	7	100.0	7	2 B39127	phosphotransferase
28	7	100.0	7	2 S25266	pile protein - Esc
29	7	100.0	7	2 A44428	'platelet aggregati

30	7	100.0	7	2 A25269	sex pheromone cAM3
31	7	100.0	7	2 A30812	sex pheromone cCF1
32	7	100.0	7	2 S42407	gramicidin S synth
33	7	100.0	7	2 A28709	phosphonacetaldeh
34	7	100.0	7	2 I40504	hypothetical prote
35	7	100.0	7	2 S17976	glucose isomerase
36	7	100.0	7	2 S38516	mablin II chain
37	7	100.0	7	2 PT0087	ribulose-bisphosph
38	7	100.0	7	2 B34818	vicilin 57K chain
39	7	100.0	7	2 A34818	vicilin 72K chain
40	7	100.0	7	2 E61491	seed protein ws-5
41	7	100.0	7	2 B33882	cadmium-binding he
42	7	100.0	7	2 FN0150	omega-gliadin 1'
43	7	100.0	7	2 PS0254	18K protein 5507 -
44	7	100.0	7	2 PQ0727	H2 class I protein
45	7	100.0	7	2 PQ0728	unidentified 5.0/1

ALIGNMENTS

RESULT 1

XEYDGD

galactose oxidase inhibitor - fungus (Cladobotryum dendroides)

C;Species: Cladobotryum dendroides

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993

C;Accession: A01341

R;Avigad, G.; Markus, Z.

Fed. Proc. 31, 447, 1972

A;Reference number: A01341

A;Accession: A01341

A;Molecule type: protein

A;Residues: 1-7 <AVI>

C;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose ox

apoenzyme, may inactivate the enzyme by binding to its prosthetic copper group.

C;Superfamily: galactose oxidase inhibitor

C;Keywords: copper

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7

Db 1 AGQNTES 7

RESULT 2

NYPG7

hypothalamic heptapeptide - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 23-Aug-1996

C;Accession: A01417

R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Safran, M.; Kong

Horm. Metab. Res. 13, 228-232, 1981

A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-relea

A;Reference number: A01417; MUID:81213980; PMID:6263778

A;Accession: A01417

A;Molecule type: protein

A;Residues: 1-7 <CHA>

C;Superfamily: hypothalamic heptapeptide

C;Keywords: hypothalamus

Query Match

Best Local Similarity 100.0%; Score 7; DB 1; Length 7;

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7

Db 1 FIYHSYK 7

RESULT 3

A61324
 dermorphin - Rohde's leaf frog
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C;Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C;Accession: A61324
 R;Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.
 Int. J. Pept. Protein Res. 17, 316-321, 1981
 A;Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Brazilian tree frog Phyllomedusa rohdei
 A;Reference number: A61324; MUID:82029915; PMID:7287302
 A;Accession: A61324
 A;Molecule type: protein
 A;Residues: 1-7 <MON>
 C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
 C;Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin
 F;2/Modified site: D-alanine (Ala) #status experimental
 F;6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F;7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 YAFGYPS 7

RESULT 4
 A60139
 fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
 C;Accession: A60139
 R;Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
 Biochim. Biophys. Acta 828, 380-382, 1985
 A;Title: Amino acid sequence around the reactive serine residue of the thioesterase domain of rat fatty-acid synthase
 A;Reference number: A60139; MUID:85175165; PMID:3921056
 A;Accession: A60139
 A;Molecule type: protein
 A;Residues: 1-7 <HAR>
 C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homologase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] synthase homology; short-chain alcohol dehydrogenase homology; coenzyme A; homodimer; multifunctional enzyme
 C;Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enzyme
 F;5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 VAGYSYG 7

RESULT 5
 S71867
 glutathione transferase (EC 2.5.1.18) class alpha 5 - pig (fragment)
 N;Alternate names: glutathione S-transferase class alpha 5
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C;Accession: S71867
 R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
 Biochem. J. 317, 879-884, 1996
 A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrophoresis
 A;Reference number: S71867; MUID:96332484; PMID:8760377
 A;Accession: S71867
 A;Molecule type: protein
 A;Residues: 1-7 <ROU>
 C;Comment: At least five species-independent classes of cytosolic glutathione transferases
 C;Superfamily: glutathione transferase
 C;Keywords: dimer; transferase

A;Pathway: detoxification; xenobiotics metabolism
 A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
 es of damage
 C;Superfamily: glutathione transferase
 C;Keywords: dimer; transferase

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 AILNYIA 7

RESULT 6
 S71870
 glutathione transferase (EC 2.5.1.18) class mu 9 - pig (fragment)
 N;Alternate names: glutathione S-transferase class mu 9
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 07-May-1999
 C;Accession: S71870
 R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
 Biochem. J. 317, 879-884, 1996
 A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrophoresis
 A;Reference number: S71864; MUID:96332484; PMID:8760377
 A;Accession: S71870
 A;Molecule type: protein
 A;Residues: 1-7 <ROU>
 C;Comment: At least five species-independent classes of cytosolic glutathione transferases
 C;Superfamily: glutathione transferase
 C;Keywords: dimer

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 SMILGYA 7

RESULT 7
 JN0859
 peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
 C;Species: Sarda orientalis (striped bonito)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C;Accession: JN0859
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide from the bonito Sarda orientalis
 A;Reference number: JN0859; MUID:94080036; PMID:7764272
 A;Accession: JN0859
 A;Molecule type: protein
 A;Residues: 1-7 <MAT>
 A;Experimental source: intestine
 C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory peptide
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7

```
Db          1 SVAKLEK 7
          :::::
RESULT 8
A60224
Met-enkephalin-Arg-Phe - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C:Accession: A60224
R:Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makk, G.; Weber, E.
J. Neurochem. 56, 1914-1920, 1991
A:Title: Isolation and characterization of opioid peptides from rabbit cerebellum.
A:Reference number: A60224; MUID:91225680; PMID:2027006
A:Accession: A60224
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NAD>
C:Superfamily: proenkephalin
C:Keywords: neuropeptide; opioid peptide

Query Match          100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY          1 XXXXXXXX 7
          :::::
Db          1 YGFMRF 7

RESULT 9
S36662
dermorphin (Lys-7) [validated] - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
C:Accession: S36662
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S36662
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIG>
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match          100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY          1 XXXXXXXX 7
          :::::
Db          1 YAFGYPK 7

RESULT 10
S21230
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C:Accession: S21230
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S21230
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIG>
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match          100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY          1 XXXXXXXX 7
          :::::
Db          1 YAFGYPK 7

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY          1 XXXXXXXX 7
          :::::
Db          1 YAFWYPN 7

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
PH1408
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PH1408; PH1405
R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.;
J. Exp. Med. 176, 1209-1214, 1992
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement i
ia virus.
A:Reference number: PH1403; MUID:93018837; PMID:1402663
A:Accession: PH1408
A:Molecule type: DNA
A:Residues: 1-7 <SHI>
A:Experimental source: clone micro m+ 46-12-2
A:Accession: PH1405
A:Molecule type: DNA
A:Residues: 1-7 <SHI2>
A:Experimental source: clone micro m+ 46-6
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY          1 XXXXXXXX 7
          :::::
Db          1 FCARRFP 7

RESULT 12
S19630
ribosomal protein L30 - Streptomyces griseus (fragment)
C:Species: Streptomyces griseus
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C:Accession: S19630
R:Ochi, K.
Int. J. Syst. Bacteriol. 42, 144-150, 1992
A:Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete
A:Reference number: S19630; MUID:92144363; PMID:1736962
A:Accession: S19630
A:Molecule type: protein
A:Residues: 1-7 <OCH>
A:Experimental source: strain IFO 13189
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

Query Match          100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY          1 XXXXXXXX 7
          :::::
Db          1 ARLKITQ 7

RESULT 13
S16364
opacity protein P.IIe - Neisseria gonorrhoeae (strain FA1090) (fragment)
N:Alternate names: outer membrane protein P.IIe
C:Species: Neisseria gonorrhoeae
A:Variety: strain FA1090
C:Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: S16364
R:Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
```

Infect. Immun. 55, 2026-2031, 1987
A;Title: Antigenic and structural differences among six proteins II expressed by a single
A;Reference number: S16360; MUID:87306843; PMID:3114142
A;Accession: S16364
A;Molecule type: protein
A;Residues: 1-7 <BAR>
A;Experimental source: strain FA1090
A;Note: expression of opacity proteins is regulated by the number of translated repeats
of repeats place the start codon in frame with the rest of the protein
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-7/Product: opacity protein P.IIf (fragment) #status experimental <MAT>

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
: : : : :
Db 1 AGEDNGR 7

RESULT 14

S16365
opacity protein P.IIf - Neisseria gonorrhoeae (strain FA1090) (fragment)
N;Alternate names: outer membrane protein P.IIf
C;Species: Neisseria gonorrhoeae
A;Variety: strain FA1090
C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C;Accession: S16365
R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
Infect. Immun. 55, 2026-2031, 1987
A;Title: Antigenic and structural differences among six proteins II expressed by a single
A;Reference number: S16360; MUID:87306843; PMID:3114142
A;Accession: S16365

A;Molecule type: protein
A;Residues: 1-7 <BAR>
A;Experimental source: strain FA1090
A;Note: expression of opacity proteins is regulated by the number of translated repeats
of repeats place the start codon in frame with the rest of the protein
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-7/Product: opacity protein P.IIf (fragment) #status experimental <MAT>

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
: : : : :
Db 1 ATEDNGR 7

RESULT 15

AS8512
venom heptapeptide - cone shell (Conus imperialis)
C;Species: Conus imperialis (imperial cone)
C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 07-May-1999
C;Accession: A58512
R;Craig, A.G.; Jimenez, E.C.; Dykert, J.; Nielsen, D.B.; Gulyas, J.; Abogadie, F.C.; Pox
J. Biol. Chem. 272, 4689-4698, 1997
A;Title: A novel post-translational modification involving bromination of tryptophan. Id
A;Reference number: A58512; MUID:97184108; PMID:9030520
A;Accession: A58512

A;Molecule type: protein
A;Residues: 1-7 <CRA>
C;Superfamily: unassigned conotoxins
C;Keywords: amidated carboxyl end; bromine; pyroglutamic acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6/Modified site: 6-bromotryptophan (Trp) #status experimental
F;7/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 100.0%; Score 7; DB 2; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
: : : : :
Db 1 QCGQAWC 7

Search completed: October 28, 2003, 09:01:57
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 28, 2003, 08:57:28 ; Search time 93 Seconds
(without alignments)
19.423 Million cell updates/sec

Title: US-09-847-940B-6
Perfect score: 7
Sequence: 1 XXXXXXX 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

1:	sp_archaea:*
2:	sp_bacteria:*
3:	sp_fungi:*
4:	sp_human:*
5:	sp_invertebrate:*
6:	sp_mammal:*
7:	sp_mhc:*
8:	sp_organelle:*
9:	sp_phage:*
10:	sp_plant:*
11:	sp_rodent:*
12:	sp_virus:*
13:	sp_vertebrate:*
14:	sp_unclassified:*
15:	sp_rviro:*
16:	sp_bacteriaph:*
17:	sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	2	Q8KMS3
2	7	100.0	7	2	Q47505
3	7	100.0	7	2	P70804
4	7	100.0	7	2	O50556
5	7	100.0	7	2	Q47477
6	7	100.0	7	2	Q47029
7	7	100.0	7	2	P72081
8	7	100.0	7	2	Q54248
9	7	100.0	7	2	Q8KMS9
10	7	100.0	7	2	O34028
11	7	100.0	7	2	O07354
12	7	100.0	7	2	Q8GL12
13	7	100.0	7	2	Q8GL04
14	7	100.0	7	2	Q8GL00
15	7	100.0	7	4	Q15903
16	7	100.0	7	4	Q8NHH7

17	7	100.0	7	4	Q15897	Q15897 homo sapien
18	7	100.0	7	6	Q28742	Q28742 oryctolagus
19	7	100.0	7	8	P92214	P92214 amblyopyrum
20	7	100.0	7	8	P92393	P92393 hordeum vul
21	7	100.0	7	8	P92403	P92403 lophopyrum
22	7	100.0	7	8	P92427	P92427 peridictyon
23	7	100.0	7	8	O99182	O99182 gnatholebia
24	7	100.0	7	8	P92430	P92430 aegilops ta
25	7	100.0	7	8	P92221	P92221 bromus iner
26	7	100.0	7	8	O98866	O98866 spinacia ol
27	7	100.0	7	8	P92425	P92425 pseudoroegn
28	7	100.0	7	8	P92381	P92381 hordeum bra
29	7	100.0	7	8	P92387	P92387 henrardia p
30	7	100.0	7	8	P92210	P92210 agropyron c
31	7	100.0	7	8	P92440	P92440 thinopyrum
32	7	100.0	7	8	P92218	P92218 australopyr
33	7	100.0	7	8	P92390	P92390 heteranthel
34	7	100.0	7	8	P92372	P92372 haynaldia v
35	7	100.0	7	8	P92442	P92442 taeniatheru
36	7	100.0	7	8	P92226	P92226 crithopsis
37	7	100.0	7	8	Q8MFY6	Q8MFY6 taraxacum (
38	7	100.0	7	8	Q95945	Q95945 saccharomyc
39	7	100.0	7	8	P92385	P92385 hordeum mar
40	7	100.0	7	8	P92421	P92421 psathyrosta
41	7	100.0	7	10	P93233	P93233 lycopersico
42	7	100.0	7	10	O49223	O49223 glycine max
43	7	100.0	7	10	Q9C5B3	Q9C5B3 arabidopsis
44	7	100.0	7	10	P82445	P82445 nicotiana t
45	7	100.0	7	11	Q8K3H6	Q8K3H6 rattus norv

ALIGNMENTS

RESULT 1

Q8KMS3 PRELIMINARY; PRT; 7 AA.
AC Q8KMS3; 22, Created
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Putative MerR2 protein.
GN MERR2.
OS Klebsiella sp. LS13-39.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=143776;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS13-39;
RX MEDLINE=21604134; PubMed=11763242;
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
RT bacteria and their classification."
RL Res. Microbiol. 152:811-822(2001).
DR EMBL; AJ302776; CAC82975.1; -
SQ SEQUENCE 7 AA; 608 MW; 6DC1B5BDD87DD6F0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 MAGASTA 7

RESULT 2

Q47505 PRELIMINARY; PRT; 7 AA.
ID Q47505
AC Q47505;

GN GLYA.
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 3384;
RX MEDLINE=96355846; PubMed=8751884;
RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
Kraig E.;
RT "cis Elements and trans factors are both important in strain-specific
regulation of the leukotoxin gene in Actinobacillus
actinomycetemcomitans";
RL Infect. Immun. 64:3451-3460(1996).
DR EMBL; U51862; AAB88721.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
Db 1 MRTGNAN 7

RESULT 3
P70804
ID P70804 PRELIMINARY; PRT; 7 AA.
AC P70804;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Algt protein (Fragment).
GN Azotobacter vinelandii.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvag H., Vaila S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71BSA5A5A2D1AED0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
Db 1 CTVSSST 7

RESULT 4
O50556
ID O50556 PRELIMINARY; PRT; 7 AA.
AC O50556;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GlyA (Fragment).

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
Db 1 CTVSSST 7

GN GLYA.
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 3384;
RX MEDLINE=96355846; PubMed=8751884;
RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
Kraig E.;
RT "cis Elements and trans factors are both important in strain-specific
regulation of the leukotoxin gene in Actinobacillus
actinomycetemcomitans";
RL Infect. Immun. 64:3451-3460(1996).
DR EMBL; U51862; AAB88721.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
Db 1 NRPVYA 7

RESULT 5
Q47477
ID Q47477 PRELIMINARY; PRT; 7 AA.
AC Q47477;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Tpi protein (Fragment).
GN Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 7-7 FROM N.A.
RX MEDLINE=85203917; PubMed=3158524;
RA Hellinga H.W., Evans P.R.;
RT "Nucleotide sequence and high-level expression of the major
Escherichia coli phosphofructokinase";
RL Eur. J. Biochem. 149:363-373(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Evans P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02519; CAA26359.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
Db 1 AEAQOR 7

RESULT 6
Q47029
ID Q47029 PRELIMINARY; PRT; 7 AA.
AC Q47029;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
Db 1 AEAQOR 7

DE Aad Al protein (Fragment).
GN Aad Al.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94079349; PubMed=8257126;
RA Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
RT "Analysis of the aac(3)-Via gene encoding a novel 3'-N-
acetyltransferase";
RL Antimicrob. Agents Chemother. 37:2074-2079(1993).
DR EMBL; M88012; AAA16193.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 ITKVVGK 7

RESULT 7
P72081 ID P72081 PRELIMINARY; PRT; 7 AA.
AC P72081; 1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 3'-methylephem hydroxylase (Fragment).
GN CEFF.
OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009872; PubMed=7557411;
RA Coque J., Perez-Balarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
Liras P.;
RT "Characterization of the cmcH genes of Nocardia lactamdurans and
Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
O-carbamoyltransferase for cephamycin biosynthesis";
RL Gene 162:21-27(1995).
DR EMBL; Z21682; CAA79797.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 TMHAVTS 7

RESULT 8
Q54248 ID Q54248 PRELIMINARY; PRT; 7 AA.
AC Q54248;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RplO protein (Fragment).
GN RplO.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=20011291; PubMed=10542330;
RA Poehling S., Piepersberg W., Wehmeier U.F.;
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
N2-3-11 and interaction of the SecY protein with the SecA protein.";
RL Biochim. Biophys. Acta 1447:298-302(1999).
DR EMBL; X95915; CAA65160.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 VTVTELV 7

RESULT 9
Q8KMS9 ID Q8KMS9 PRELIMINARY; PRT; 7 AA.
AC Q8KMS9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Putative transposase (Fragment).
GN TNIA.
OS Enterobacter sp. CH2-4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=143777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH2-4;
RX MEDLINE=21604134; PubMed=11763242;
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,
Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
bacteria and their classification";
RL Res. Microbiol. 152:811-822(2001).
DR EMBL; AJ302778; CAC83058.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DAA9A0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 FDQIEEW 7

RESULT 10
Q34028 ID Q34028 PRELIMINARY; PRT; 7 AA.
AC Q34028;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Catechol-2,3-dioxygenase (Fragment).
GN PHNE.
OS Sphingomonas chungbukensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Sphingomonas.
OX NCBI_TaxID=56193;
RN [1]
RP SEQUENCE FROM N.A.

Tue Oct 28 09:28:58 2003

```
RC STRAIN=DJ77;
RA Kim Y.-C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88298; AAB66311.1; -.
KW Dioxynase.
FT NON TER 1
SQ SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 7;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
DB 1 REMTVNT 7

RESULT 11
O07354 PRELIMINARY; PRT; 7 AA.
ID O07354
AC O07354;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NIFK (Fragment).
GN NIFK.
OS Synchococcus sp. (strain PCC 8801 / RF-1) (Cyanotheca PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synchococcus sp. strain
RT RF-1."
RL Microbiology 145:743-753(1999).
DR EMBL; AF003700; AAC35193.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 7;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
DB 1 ISFDLVR 7

RESULT 12
O08GL12 PRELIMINARY; PRT; 7 AA.
ID O08GL12
AC O08GL12;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG plasmid group cp32-9.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N40;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142100; AAN17911.1; -.
KW Plasmid.

FT NON TER 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 7;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
DB 1 WIKNLK 7

RESULT 13
O08GL04 PRELIMINARY; PRT; 7 AA.
ID O08GL04
AC O08GL04;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG plasmid group cp32-5.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93-0107;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142103; AAN17848.1; -.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 7 AA; 914 MW; 6337244330504310 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 7;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
DB 1 WIKNLK 7

RESULT 14
O08GL00 PRELIMINARY; PRT; 7 AA.
ID O08GL00
AC O08GL00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG plasmid group cp32-13.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA15;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142106; AAN17857.1; -.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 7;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
: : : : :
Db 1 KWIILK 7

RESULT 15

Q15903 PRELIMINARY; PRT; 7 AA.
AC Q15903;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE (Clone XP7E7B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN {}
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32082; AAA73893.1; -.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 849 MW; 6B040339CDD33DB0 CRC64;

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
: : : : :
Db 1 AKAFKE 7

Search completed: October 28, 2003, 08:59:44
Job time : 98 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 09:01:17 ; Search time 366 Seconds
(without alignments)
3.203 Million cell updates/sec

Title: US-09-847-940B-6
Perfect score: 7
Sequence: 1 XXXXXX 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	7	US-08-765-837-7
2	7	100.0	7	7	US-08-344-824-53
3	7	100.0	7	7	US-08-996-140-4
4	7	100.0	7	7	US-08-996-140-17
5	7	100.0	7	8	US-08-859-699-14
6	7	100.0	7	8	US-08-859-699-22
7	7	100.0	7	8	US-08-812-393A-51
8	7	100.0	7	8	US-08-967-573A-4
9	7	100.0	7	8	US-08-967-573A-5
10	7	100.0	7	8	US-08-967-573A-12
11	7	100.0	7	8	US-08-967-573A-13
12	7	100.0	7	8	US-08-967-573A-14
13	7	100.0	7	8	US-08-967-573A-15
14	7	100.0	7	8	US-08-967-573A-16
15	7	100.0	7	8	US-08-967-573A-17

16	7	100.0	7	8	US-08-967-573A-18	Sequence 18, Appl
17	7	100.0	7	8	US-08-967-573A-19	Sequence 19, Appl
18	7	100.0	7	8	US-08-967-573A-20	Sequence 20, Appl
19	7	100.0	7	8	US-08-967-573A-21	Sequence 21, Appl
20	7	100.0	7	8	US-08-967-573A-22	Sequence 22, Appl
21	7	100.0	7	8	US-08-801-405B-2	Sequence 2, Appl
22	7	100.0	7	8	US-08-881-509-42	Sequence 42, Appl
23	7	100.0	7	8	US-08-450-842-80	Sequence 80, Appl
24	7	100.0	7	8	US-08-450-842-82	Sequence 82, Appl
25	7	100.0	7	8	US-08-987-756-1	Sequence 1, Appl
26	7	100.0	7	8	US-08-987-756-3	Sequence 3, Appl
27	7	100.0	7	8	US-08-681-219-2	Sequence 23, Appl
28	7	100.0	7	8	US-08-681-219-23	Sequence 3, Appl
29	7	100.0	7	8	US-08-873-601-3	Sequence 1, Appl
30	7	100.0	7	8	US-08-871-076-1	Sequence 39, Appl
31	7	100.0	7	8	US-08-981-824-39	Sequence 41, Appl
32	7	100.0	7	8	US-08-981-824-41	Sequence 7, Appl
33	7	100.0	7	8	US-08-592-711-7	Sequence 10, Appl
34	7	100.0	7	8	US-08-592-711-10	Sequence 11, Appl
35	7	100.0	7	8	US-08-592-711-11	Sequence 232, App
36	7	100.0	7	8	US-08-424-550B-232	Sequence 290, App
37	7	100.0	7	8	US-08-424-550B-290	Sequence 325, App
38	7	100.0	7	8	US-08-424-550B-325	Sequence 355, App
39	7	100.0	7	8	US-08-424-550B-355	Sequence 359, App
40	7	100.0	7	8	US-08-424-550B-359	Sequence 370, App
41	7	100.0	7	8	US-08-424-550B-370	Sequence 378, App
42	7	100.0	7	8	US-08-424-550B-378	Sequence 489, App
43	7	100.0	7	8	US-08-424-550B-489	Sequence 497, App
44	7	100.0	7	8	US-08-424-550B-497	Sequence 518, App
45	7	100.0	7	8	US-08-424-550B-518	

ALIGNMENTS

RESULT 1
US-08-765-837-7
; Sequence 7, Application US/08765837
; Publication No. US20030147900A1
; GENERAL INFORMATION:
; APPLICANT: LAUB, RUTH
; APPLICANT: DI GIAMBATTISTA, MARIO
; TITLE OF INVENTION: ANTIGENIC POLYPEPTIDE SEQUENCE
; TITLE OF INVENTION: OF FACTOR VIII, AND FRAGMENTS AND/OR
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,837
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/BE95/00068
; FILING DATE: 14-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA48.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. US20030147900A1e
 FRAGMENT TYPE: internal
 US-08-765-837-7

Query Match 100.0%; Score 7; DB 7; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 ETKSWYF 7

RESULT 2

US-08-344-824-53
 Sequence 53, Application US/08344824
 Publication No. US20030152580A1

GENERAL INFORMATION:
 APPLICANT: SETTE, Alessandro
 APPLICANT: SIDNEY, John
 TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
 NUMBER OF SEQUENCES: 399
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Steuart Street Tower, 20th
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,824
 FILING DATE: 23-NOV-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/278,634
 FILING DATE: 21-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 14137-80-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-344-824-53

Query Match 100.0%; Score 7; DB 7; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 LTWYFW 7

RESULT 3

US-08-996-140-4
 Sequence 4, Application US/08996140
 Publication No. US20030190318A1
 GENERAL INFORMATION:
 APPLICANT: TORIGOE, Kakuji
 APPLICANT: USHIO, Shimpel
 APPLICANT: KUNIKATA, Toshio
 APPLICANT: KURIMOTO, Masashi
 TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,140
 FILING DATE: 22-DEC-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 356,426/1996
 FILING DATE: 26-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 52,526/1997
 FILING DATE: 21-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 163,490/1997
 FILING DATE: 6-JUN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 215,490/1997
 FILING DATE: 28-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: TORIGOE-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal fragment
 US-08-996-140-4

Query Match 100.0%; Score 7; DB 7; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 IMTEPG 7

RESULT 4

US-08-996-140-17
 Sequence 17, Application US/08996140
 Publication No. US20030190318A1

GENERAL INFORMATION:
 APPLICANT: TORIGOE, Kakuji
 APPLICANT: USHIO, Shimpel
 APPLICANT: KUNIKATA, Toshio
 APPLICANT: KURIMOTO, Masashi
 TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
 NUMBER OF SEQUENCES: 31

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/996,140
;; FILING DATE: 22-DEC-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 356,426/1996
;; FILING DATE: 26-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 52,526/1997
;; FILING DATE: 21-FEB-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 163,490/1997
;; FILING DATE: 6-JUN-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 215,490/1997
;; FILING DATE: 28-JUL-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: TORIGOE=2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
US-08-996-140-17

Query Match 100.0%; Score 7; DB 7; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 NAKTLAD 7

RESULT 5
US-08-859-699-14
; Sequence 14, Application US/08859699A
; Publication No. US20010007017A1
; GENERAL INFORMATION:
; APPLICANT: VELJKOVIC, Veljko
; APPLICANT: METLAS, Radmila
; TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTIBODY REPRESENTING THE
; TITLE OF INVENTION: PROGNOSTIC MARKER FOR HIV DISEASE PROGRESSION
; FILE REFERENCE: VELJKOVIC et al. 08/859,699
; CURRENT APPLICATION NUMBER: US/08/859,699A
; CURRENT FILING DATE: 1997-05-21
; EARLIER FILING DATE: 1996-05-22
; EARLIER FILING DATE: 1996-05-22
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:Derivative of
;; OTHER INFORMATION: NTM peptide.
US-08-859-699-14

Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 KTIHQL 7

RESULT 6
US-08-859-699-22
; Sequence 22, Application US/08859699A
; Publication No. US20010007017A1
; GENERAL INFORMATION:
; APPLICANT: VELJKOVIC, Veljko
; APPLICANT: METLAS, Radmila
; TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTIBODY REPRESENTING THE
; TITLE OF INVENTION: PROGNOSTIC MARKER FOR HIV DISEASE PROGRESSION
; FILE REFERENCE: VELJKOVIC et al. 08/859,699
; CURRENT APPLICATION NUMBER: US/08/859,699A
; CURRENT FILING DATE: 1997-05-21
; EARLIER FILING DATE: 1996-05-22
; EARLIER FILING DATE: 1996-05-22
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Derivative of
; OTHER INFORMATION: NTM peptide.
US-08-859-699-22

Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 IVQLQES 7

RESULT 7
US-08-812-393A-51
; Sequence 51, Application US/08812393A
; Publication No. US20010007152A1
; GENERAL INFORMATION:
; APPLICANT: SHERMAN, Linda A.
; APPLICANT: LUSTGARTEN, Joseph
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING
; TITLE OF INVENTION: T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR
; TITLE OF INVENTION: ANTIGENS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

INFORMATION FOR SEO ID NO: 4:

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RESULT 10
US-08-967-573A-12
; Sequence 12, Application US/08967573A
; Publication No. US20010048926A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
; TITLE OF INVENTION: FOR DENTAL CARRIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,573A
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/057,162
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/877,295
; FILING DATE: 01-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-12
Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
Db 1 GGYEFLL 7

RESULT 11
US-08-967-573A-13
; Sequence 13, Application US/08967573A
; Publication No. US20010048926A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
; TITLE OF INVENTION: FOR DENTAL CARRIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
```

```
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,573A
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/057,162
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/877,295
; FILING DATE: 01-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-13
Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
Db 1 GYEFLLA 7

RESULT 12
US-08-967-573A-14
; Sequence 14, Application US/08967573A
; Publication No. US20010048926A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
; TITLE OF INVENTION: FOR DENTAL CARRIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,573A
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/057,162
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/877,295
; FILING DATE: 01-MAY-1992
```

Tue Oct 28 09:28:57 2003

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; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-14

Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 EFLAND 7

RESULT 14
US-08-967-573A-16
; Sequence 16, Application US/08967573A
; Publication No. US20010048926A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
; TITLE OF INVENTION: FOR DENTAL CARRIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,573A
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/057,162
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/877,295
; FILING DATE: 01-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-16

Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 LANDVDN 7

RESULT 15
US-08-967-573A-17
; Sequence 17, Application US/08967573A
; Publication No. US20010048926A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
; TITLE OF INVENTION: FOR DENTAL CARRIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,573A
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/057,162
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/877,295
; FILING DATE: 01-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-15

; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-14

Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 YEFLAN 7

RESULT 13
US-08-967-573A-15
; Sequence 15, Application US/08967573A
; Publication No. US20010048926A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
; TITLE OF INVENTION: FOR DENTAL CARRIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,573A
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/057,162
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/877,295
; FILING DATE: 01-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-15
```

APPLICANT: Taubman, Martin A.
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
TITLE OF INVENTION: FOR DENTAL CARRIES
NUMBER OF SEQUENCES: 22
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: FDC92-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-967-573A-17

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
: : : : :
Db 1 ANDVDNS 7

Search completed: October 28, 2003, 09:17:12
Job time : 366 secs

PD 3/2/2010
a 8/22/2000

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 08:57:28 ; Search time 81 Seconds
(without alignments)
13.717 Million cell updates/sec

Title: US-09-847-940B-6
Perfect score: 7
Sequence: 1 XXXXXX 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	2	Sequence of thymos
2	7	100.0	7	2	Sequence which cor
3	7	100.0	7	2	Sequence of peptid
4	7	100.0	7	2	Sequence of enceph
5	7	100.0	7	2	Sequence of cyclic
6	7	100.0	7	2	Sequence of peptid
7	7	100.0	7	2	Sequence of peptid
8	7	100.0	7	2	Peptide secretin d
9	7	100.0	7	2	Analgesic peptide

10	7	100.0	7	2	Analgesic peptide
11	7	100.0	7	2	Analgesic peptide
12	7	100.0	7	2	Analgesic peptide
13	7	100.0	7	2	Analgesic peptide
14	7	100.0	7	2	Analgesic peptide
15	7	100.0	7	2	Analgesic peptide
16	7	100.0	7	2	Analgesic peptide
17	7	100.0	7	2	Analgesic peptide
18	7	100.0	7	2	Analgesic peptide
19	7	100.0	7	2	Analgesic peptide
20	7	100.0	7	2	Analgesic peptide
21	7	100.0	7	2	Analgesic peptide
22	7	100.0	7	2	Analgesic peptide
23	7	100.0	7	2	Analgesic peptide
24	7	100.0	7	2	Analgesic peptide
25	7	100.0	7	2	Analgesic peptide
26	7	100.0	7	2	Analgesic peptide
27	7	100.0	7	2	Analgesic peptide
28	7	100.0	7	2	Analgesic peptide
29	7	100.0	7	2	Analgesic peptide
30	7	100.0	7	2	Analgesic peptide
31	7	100.0	7	2	Analgesic peptide
32	7	100.0	7	2	Analgesic peptide
33	7	100.0	7	2	Analgesic peptide
34	7	100.0	7	2	Analgesic peptide
35	7	100.0	7	2	Analgesic peptide
36	7	100.0	7	2	Analgesic peptide
37	7	100.0	7	2	Analgesic peptide
38	7	100.0	7	2	Analgesic peptide
39	7	100.0	7	2	Analgesic peptide
40	7	100.0	7	2	Analgesic peptide
41	7	100.0	7	2	Analgesic peptide
42	7	100.0	7	2	Analgesic peptide
43	7	100.0	7	2	Analgesic peptide
44	7	100.0	7	2	Analgesic peptide
45	7	100.0	7	2	Analgesic peptide

ALIGNMENTS

RESULT 1

AAP10061

ID AAP10061 standard; peptide; 7 AA.

XX AAP10061;

AC AAP10061;

XX 25-MAR-2003 (updated)

DT 16-AUG-2002 (updated)

DT 12-AUG-1992 (first entry)

XX Sequence of thymosin alpha-1 peptide fragment III.

DE Sequence of thymosin alpha-1 peptide fragment III.

XX Immunostimulant; immunoregulator; immune deficiency disease;

KW viral infection.

XX Unidentified.

OS Unidentified.

XX EP33384-A.

XX 12-AUG-1981.

XX 17-DEC-1980; 80EP-0107997.

XX 25-MAR-1980; 80US-0133708.

PR 02-APR-1984; 84US-0595730.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Birr C, Stollenwerk U, Werner I;

XX WPI; 1981-60683D/34.

PT Immunostimulant medicaments contg. thymosin. alpha-1 peptide
PT fragment - e.g. seryl-aspartyl-alanyl-alanyl -valyl-aspartic acid
XX
PS Claim 26; Page 53; 68pp; German.
XX
CC The inventors claim new medicaments with immunostimulant activity.
CC They contain at least one thymosin alpha-1 fragment and/or
CC derivative. The N-terminal of the fragments carry a 1-6 C acyl or
CC (1-6 C acyl)-glycyl gp. The Glu residues may be present as amides
CC or 1-6 C alkylamides and/or the asparagine or aspartic-acid residues
CC are present as the amide, 1-6 C alkyl-amide, diamide or di(1-6 C
CC alkyl amide).
CC (Updated on 16-AUG-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XXXXXXX 7
Db 1 TKDLKEK 7
RESULT 2
AAP10170
ID AAP10170 standard; peptide; 7 AA.
XX
AC AAP10170;
XX
DT 19-AUG-1992 (first entry)
XX
DE Sequence which corresp. to AAs 325-332 of the C4 isozyme of lactate
DE dehydrogenase found in mammalian sperm.
XX
KW Vaccine; contraceptive; fertility reduction.
XX
OS Mammal.
XX
XX US4290944-A.
XX
PD 22-SEP-1981.
XX
PF 31-JUL-1980; 80US-0174011.
XX
PR 31-JUL-1980; 80US-0174011.
PR 21-SEP-1981; 81WO-US01271.
PR 01-JAN-1981; 81AU-0076469.
PR 21-SEP-1981; 81EP-0902712.
PR 01-JAN-1981; 81JP-0503235.
PR 11-MAY-1983; 83DK-0002120.
PR 16-SEP-1981; 81CA-0386008.
XX
PA (NOUN) NORTHWESTERN UNIV.
PA (GOLD/) GOLDBERG E.
XX
PI Goldber E;
XX
XX WPI; 1981-75566D/41 (75566D).
XX
DR Antigenic linear hexa:peptide - useful for conjugation to protein
PT carrier for vaccine to reduce fertility of mammals
XX
PS Claim 1; column 4; 3pp; English.
XX
CC The peptide of the invention is an antigen for use in a vaccine for
CC reducing the fertility of mammals. It is conjugated to a carrier
CC molecule, pref. a protein which itself elicits an antigenic response
CC and can be safely administered, e.g. to tetanus toxoid for
CC intramuscular admin., pref. to human females, when antibodies are

CC formed and appear in the oviduct fluid. Dose is 1-10 mg.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XXXXXXX 7
Db 1 MQKDLEL 7
RESULT 3
AAP10099
ID AAP10099 standard; peptide; 7 AA.
XX
AC AAP10099;
XX
DT 25-OCT-1992 (first entry)
XX
DE Sequence of peptides with immunopotentiating function.
XX
KW Immunopotentiating agent; thymus-dependent lymphocyte; regulation;
KW differentiation.
XX
OS Synthetic.
XX
PN EP26464-A.
XX
PD 08-APR-1981.
XX
PF 11-AUG-1982; 82EP-0407222.
XX
PR 28-APR-1980; 80US-0144516.
PR 28-SEP-1979; 79US-0079630.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
PA (SPAR-) SPARAMEDICA AG.
XX
PI Meienhofer JA;
XX
XX WPI; 1981-27641D/16 (27641D).
XX
PT Peptide derivs. contg. glutamic acid and asparagine - useful as
PT immuno-potentiating agents by effect on T-cells
XX
PS Claim 7; Page 25; 31pp; German.
XX
CC The sequence in AAP10099 is in claim 7. Preceding claims claim
CC fragments of AAP10099 comprising residues 2-7, 3-7, 4-7, 5-7 and 6-7.
CC AAP10099 and its fragments and their pharmaceutically acceptable salts
CC influence the regulation, differentiation and function of thymus-
CC dependent lymphocytes, and so are useful as immunopotentiating
CC agents when administered parenterally at 0.1-50 mg./kg. The tri- and
CC penta-peptide fragments are esp. pref. cpds.
XX
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
QY 1 XXXXXXX 7
Db 1 VVEEAEN 7
RESULT 4
AAP10156
ID AAP10156 standard; peptide; 7 AA.
XX
AC AAP10156;

PR 10-SEP-1979; 79DE-2936543.
 XX (BEHW) BEHRINGWERKE AG.
 PA Karges HE, Heber H, Uhmman R, Teetz V, Geiger R;
 PI WPI; 1981-21810D/13.
 XX Chromogenic peptide derivs. - useful for determ. of hydrolytic
 PT enzymes or inhibitors
 XX Disclosure; Table 1, page 11; 37pp; German.
 PS The compounds in Table 1 exemplify the chromogenic peptide derivs.
 XX of the invention. They can be prep'd. by standard peptide synthesis
 CC methods, e.g. by coupling suitably protected derivs. of W-P-OH and
 CC H-B-X-NHR and then removing the protecting gps.. They are useful as
 CC reagents for determ. of hydrolytic enzymes or enzyme inhibitors,
 CC esp. of proteases in body fluids. They are more specific (less
 CC sensitive to esterases) than prior art chromogenic substrates.
 CC

XX Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
 Db 1 EGGVRY 7

RESULT 8
 AAP10368
 ID AAP10368 standard; Protein; 7 AA.
 XX
 AC AAP10368;
 XX
 DT 16-DEC-1992 (first entry)
 XX
 DE Peptide secretin derivative #7.
 XX
 KW secretin; insulin; diabetes; pancreas; islets of langerhans; glucose.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Modified-site 5
 FT /label= OTHER
 FT /note= "pyroglutamic acid"
 FT Misc-difference 7
 FT /label= OTHER
 FT /note= "OR3 or -NR1R2
 FT where R1 and R2 are H, C1-C6 alkyl,
 FT C3-C8 cycloalkyl. R1 and R2 may also be
 FT linked together to form a cyclic gp having
 FT at least 1 hetero atom ie the amide bonded N,
 FT opt. contg. an additional hetero atom eg. N,
 FT O, or S.
 FT where R3 is H, C1-C6 alkyl, C3-C8 cycloalkyl,
 FT benzyl, phenacyl, phthalimidomethyl,
 FT beta-methylthioethyl, 4-picolyl, and benzyl
 FT substituted with nitro, methoxy, methyl,
 FT halogen."

XX US4265884-A.
 PN
 XX
 PD 05-MAY-1981.
 XX
 PF 24-SEP-1979; 79US-0078425.
 XX
 PR 05-SEP-1979; 79DK-0003710.
 PR 28-SEP-1978; 78DK-0004304.
 XX
 PA (NORI) NORDISK INSULINLAB.
 XX
 PI Kofod H;
 XX
 DR WPI; 1981-38054D/21 (38054D).
 XX
 PT Secretin related polypeptide(s) - which potentiate glucose
 PT stimulated secretion of insulin
 XX
 PS Claim 2; Column 6; 4pp; English.
 XX
 CC This peptide is a derivative of the intestinal hormone secretin.
 CC They potentiate the glucose stimulated secretion of insulin from
 CC Langerhans' islets. They may be used to treat diabetics who have

PR 10-SEP-1979; 79DE-2936543.
 XX (BEHW) BEHRINGWERKE AG.
 PA Karges HE, Heber H, Uhmman R, Teetz V, Geiger R;
 PI WPI; 1981-21810D/13.
 XX Chromogenic peptide derivs. - useful for determ. of hydrolytic
 PT enzymes or inhibitors
 XX Disclosure; Table 1, page 11; 37pp; German.
 PS The compounds in Table 1 exemplify the chromogenic peptide derivs.
 XX of the invention. They can be prep'd. by standard peptide synthesis
 CC methods, e.g. by coupling suitably protected derivs. of W-P-OH and
 CC H-B-X-NHR and then removing the protecting gps.. They are useful as
 CC reagents for determ. of hydrolytic enzymes or enzyme inhibitors,
 CC esp. of proteases in body fluids. They are more specific (less
 CC sensitive to esterases) than prior art chromogenic substrates.
 CC

XX Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
 Db 1 GGPEGRF 7

RESULT 7
 AAP10088
 ID AAP10088 standard; peptide; 7 AA.
 XX
 AC AAP10088;
 XX
 DT 12-OCT-1992 (first entry)
 XX
 DE Sequence of peptide in chromogenic compound.
 XX
 KW Hydrolytic enzyme determinant; enzyme inhibitor.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Modified-site 1
 FT /label= C4H9-CO-Ala
 FT Modified-site 7
 FT /label= Tyr-p-Nitranilid

XX EP25190-A.
 PN
 XX
 PD 18-MAR-1981.
 XX
 PF 28-AUG-1980; 80EP-0105113.
 XX
 PR 10-SEP-1979; 79DE-2936543.
 XX
 PA (BEHW) BEHRINGWERKE AG.
 XX
 PI Karges HE, Heber H, Uhmman R, Teetz V, Geiger R;
 XX
 DR WPI; 1981-21810D/13.
 XX
 PT Chromogenic peptide derivs. - useful for determ. of hydrolytic
 PT enzymes or inhibitors
 XX
 PS Disclosure; Table 1, page 11; 37pp; German.
 XX
 CC The compounds in Table 1 exemplify the chromogenic peptide derivs.
 CC of the invention. They can be prep'd. by standard peptide synthesis

CC themselves lost the ability to liberate insulin from the Langerhans
 CC islets.

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 SARLZRL 7

RESULT 9
 AAP10583
 ID AAP10583 standard; peptide; 7 AA.

XX AC AAP10583;

XX DT 25-MAR-2003 (updated)
 XX DT 22-DEC-1992 (first entry)

XX DE Analgesic peptide #39.

XX KW Growth Hormone release; prolactin; painkiller; anti-psychotic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 2 /note= "D-Ala"

FT Modified-site 5 /note= "Bzl-protected if Ser at position 7
 is Bzl-protected"

FT Modified-site 6 /label= OTHER

FT Modified-site 7 /note= "hydroxyproline"

FT Modified-site 7 /note= "Ser-NH2 or Ser(Bzl)-NH2 if Tyr at
 position 5 is Bzl-protected"

XX PN BE885283-A.

XX PD 18-MAR-1981.

XX PF 19-SEP-1980; 80BE-0983143.

XX PR 09-MAY-1980; 80GB-0015412.

XX PR 20-SEP-1979; 79GB-0032590.

XX PR 20-SEP-1978; 78GB-0032590.

XX PR 17-SEP-1980; 80GB-0029999.

XX (FARM) FARMITALIA ERBA SPA CARLO.

XX PI Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;

XX DR WPI; 1981-23404D/14 (23404D).

XX PT Analgesic and antipsychotic polypeptide(s) - also useful in neuro
 endocrinology and to stimulate liberation of growth hormone and
 prolactin

XX PS Example; Page 14; 41pp; French.

XX CC Peptides covered by this sequence are preferred examples of a highly
 generic formula for peptides with analgesic and antipsychotic
 properties. The peptides also have Growth Hormone releasing and
 prolactin releasing properties. See AAP10545-P10584.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 YAFPYPS 7

RESULT 10

AAP10530
 ID AAP10530 standard; peptide; 7 AA.

XX AC AAP10530;

XX DT 25-MAR-2003 (updated)

XX DT 22-DEC-1992 (first entry)

XX DE Analgesic peptide #41.

XX KW Growth Hormone release; prolactin; painkiller; anti-psychotic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "opt. Boc-protected"

FT Misc-difference 2 /note= "D-Ala"

FT Modified-site 6 /label= OTHER

FT Modified-site 7 /note= "hydroxyproline"

FT Modified-site 7 /note= "Ser-NH2, opt. Bzl-protected"

XX PN BE885283-A.

XX PD 18-MAR-1981.

XX PF 19-SEP-1980; 80BE-0983143.

XX PR 09-MAY-1980; 80GB-0015412.

XX PR 20-SEP-1979; 79GB-0032590.

XX PR 20-SEP-1978; 78GB-0032590.

XX PR 17-SEP-1980; 80GB-0029999.

XX (FARM) FARMITALIA ERBA SPA CARLO.

XX PI Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;

XX DR WPI; 1981-23404D/14 (23404D).

XX PT Analgesic and antipsychotic polypeptide(s) - also useful in neuro
 endocrinology and to stimulate liberation of growth hormone and
 prolactin

XX PS Example; Page 14; 41pp; French.

XX CC Peptides covered by this sequence are preferred examples of a highly
 generic formula for peptides with analgesic and antipsychotic
 properties. The peptides also have Growth Hormone releasing and
 prolactin releasing properties. The peptides whose N-terminus is
 not Boc-protected are in the form of their hydrochloride salts.
 CC See AAP10545-P10584.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 YAFGPPS 7

RESULT 11
AAP10564
ID AAP10564 standard; peptide; 7 AA.
XX AAP10564;
XX AC
XX DT 25-MAR-2003 (updated)
XX DT 22-DEC-1992 (first entry)
XX XX Analgesic peptide #20.
XX XX Growth Hormone release; prolactin; painkiller; anti-psychotic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "opt. Boc-protected when Ser at position 7
FT is Ser-NH2 or Ser-NHNH2"
FT Misc-difference 2 /note= "D-Ala"
FT Modified-site 5 /note= "opt. Bzl-protected when Ser at position 7
FT is Ser-NH2 or Ser(Bzl)-NH2"
FT Modified-site 7 /note= "Ser-OH, Ser-NH2, Ser-OMe, Ser-NHMe,
FT Ser-NHET, Ser-NH-CH(CH3)2, Ser-NHNH2 or
FT Ser-NHNH2"
XX BE885283-A.
XX PN
XX PD 18-MAR-1981.
XX PF 19-SEP-1980; 80BE-0983143.
XX PR 09-MAY-1980; 80GB-0015412.
XX PR 20-SEP-1979; 79GB-0032590.
XX PR 20-SEP-1978; 78GB-0032590.
XX PR 17-SEP-1980; 80GB-0029999.
XX PA (FARM) FARMITALIA ERBA SPA CARLO.
XX PI Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;
XX WPI; 1981-23404D/14 (23404D).
XX DR Analgesic and antipsychotic polypeptide(s) - also useful in neuro
XX PT endocrinology and to stimulate liberation of growth hormone and
XX PT prolactin
XX PS Example; Page 12; 4lpp; French.
XX CC Peptides covered by this sequence are preferred examples of a highly
XX CC generic formula for peptides with analgesic and antipsychotic
XX CC properties. The peptides also have Growth Hormone releasing and
XX CC prolactin releasing properties. Peptides whose N-terminus is not
XX CC Boc-protected and whose C-terminus is Ser-NH2 may be in
XX CC the form of their hydrochloride or trifluoroacetic acid salts; the
XX CC peptide with Ser-NHNH2 at position 7 and lacking a Boc-protecting
XX CC group at the N-terminus is in the form of its hydrochloride salt
XX CC and the peptides with Ser-OMe, Ser-OH, Ser-NHMe or Ser-NHET at
XX CC position 7 are in the form of their hydrochloride salts.
XX CC See AAP10545-P10584.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 YAFGPPS 7

RESULT 12
AAP10565
ID AAP10565 standard; peptide; 7 AA.
XX AAP10565;
XX AC
XX DT 25-MAR-2003 (updated)
XX DT 22-DEC-1992 (first entry)
XX XX Analgesic peptide #21.
XX XX Growth Hormone release; prolactin; painkiller; anti-psychotic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "opt. Boc-protected"
FT Misc-difference 2 /note= "D-Ala"
FT Modified-site 7 /note= "Ser-NH2"
XX BE885283-A.
XX PN
XX PD 18-MAR-1981.
XX PF 19-SEP-1980; 80BE-0983143.
XX PR 09-MAY-1980; 80GB-0015412.
XX PR 20-SEP-1979; 79GB-0032590.
XX PR 20-SEP-1978; 78GB-0032590.
XX PR 17-SEP-1980; 80GB-0029999.
XX PA (FARM) FARMITALIA ERBA SPA CARLO.
XX PI Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;
XX WPI; 1981-23404D/14 (23404D).
XX DR Analgesic and antipsychotic polypeptide(s) - also useful in neuro
XX PT endocrinology and to stimulate liberation of growth hormone and
XX PT prolactin
XX PS Example; Page 13; 4lpp; French.
XX CC Peptides covered by this sequence are preferred examples of a highly
XX CC generic formula for peptides with analgesic and antipsychotic
XX CC properties. The peptides also have Growth Hormone releasing and
XX CC prolactin releasing properties. The peptide whose N-terminus is not
XX CC Boc-protected is in the form of its hydrochloride salt.
XX CC See AAP10545-P10584.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 YAFGPPS 7

Db 1 YAFGPPS 7

RESULT 13

AAP10566
ID AAP10566 standard; peptide; 7 AA.

XX AC AAP10566;
XX DT 25-MAR-2003 (updated)
XX DT 22-DEC-1992 (first entry)
XX DE Analgesic peptide #22.
XX KW Growth Hormone release; prolactin; painkiller; anti-psychotic.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "opt. Boc-protected"
XX FT Misc-difference 2 /note= "D-Ala"
XX FT Modified-site 7 /note= "Ser-NH2"

BE885283-A.

18-MAR-1981.

19-SEP-1980; 80BE-0983143.

09-MAY-1980; 80GB-0015412.

20-SEP-1979; 79GB-0032590.

20-SEP-1978; 78GB-0032590.

17-SEP-1980; 80GB-0029999.

(FARM) FARMITALIA ERBA SPA CARLO.

Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;

WPI; 1981-23404D/14 (23404D).

XX Analgesic and antipsychotic polypeptide(s) - also useful in neuro
XX endocrinology and to stimulate liberation of growth hormone and
XX prolactin

Example; Page 13; 4lpp; French.

XX Peptides covered by this sequence are preferred examples of a highly
XX generic formula for peptides with analgesic and antipsychotic
XX properties. The peptides also have Growth Hormone releasing and
XX prolactin releasing properties. The peptide whose N-terminus is not
XX Boc-protected is in the form of its hydrochloride salt.

XX See AAP10545-P10584.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7

Db 1 YAFGWPS 7
: : : : :
: : : : :

RESULT 14

AAP10567
ID AAP10567 standard; peptide; 7 AA.

AC AAP10567;

XX DT 25-MAR-2003 (updated)
XX DT 22-DEC-1992 (first entry)

XX DE Analgesic peptide #23.

XX KW Growth Hormone release; prolactin; painkiller; anti-psychotic.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Misc-difference 2 /note= "D-Ala"
XX FT Modified-site 7 /note= "Ser-NH2"

BE885283-A.

18-MAR-1981.

19-SEP-1980; 80BE-0983143.

09-MAY-1980; 80GB-0015412.

20-SEP-1979; 79GB-0032590.

20-SEP-1978; 78GB-0032590.

17-SEP-1980; 80GB-0029999.

(FARM) FARMITALIA ERBA SPA CARLO.

Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;

WPI; 1981-23404D/14 (23404D).

XX Analgesic and antipsychotic polypeptide(s) - also useful in neuro
XX endocrinology and to stimulate liberation of growth hormone and
XX prolactin

Example; Page 13; 4lpp; French.

XX This peptide, which is in the form of its hydrochloride salt, is a
XX preferred example of a highly generic formula for peptides with
XX analgesic and antipsychotic properties. The peptides also have
XX Growth Hormone releasing and prolactin releasing properties.

XX See AAP10545-P10584.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7

Db 1 YAFGPPS 7
: : : : :
: : : : :

RESULT 15

AAP10568
ID AAP10568 standard; peptide; 7 AA.

XX AC AAP10568;

XX DT 25-MAR-2003 (updated)
XX DT 22-DEC-1992 (first entry)

XX DE Analgesic peptide #24.

XX KW Growth Hormone release; prolactin; painkiller; anti-psychotic.
XX OS Synthetic.

```
XX Key Location/Qualifiers
FH Misc-difference 2 /note= "D-Ala"
FT Modified-site 5
FT Modified-site 7 /note= "Phe(NO2) or p-fluorophe"
FT Modified-site 7 /note= "Ser-NH2"
XX
PN BE885283-A.
XX
PD 18-MAR-1981.
XX
PF 19-SEP-1980; 80BE-0983143.
XX
PR 09-MAY-1980; 80GB-0015412.
PR 20-SEP-1979; 79GB-0032590.
PR 20-SEP-1978; 78GB-0032590.
PR 17-SEP-1980; 80GB-0029999.
XX
PA (FARM ) FARMITALIA ERBA SPA CARLO.
XX
PI Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;
XX
DR WPI; 1981-23404D/14 (23404D).
XX
PT Analgesic and antipsychotic polypeptide(s) - also useful in neuro
PT endocrinology and to stimulate liberation of growth hormone and
PT prolactin
XX
PS Example; Page 13; 41pp; French.
XX
CC Peptides covered by this sequence are preferred examples of a highly
CC generic formula for peptides with analgesic and antipsychotic
CC properties. The peptides also have Growth Hormone releasing and
CC prolactin releasing properties. The peptide in which Phe(5) is
CC Phe(NO2) is in the form of its hydrochloride salt.
CC See AAP10545-P10584.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 YAFGPPS 7
```

Search completed: October 28, 2003, 09:01:08
Job time : 81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 08:57:27 ; Search time 22 Seconds
(without alignments)
14.963 Million cell updates/sec

Title: US-09-847-940B-6
Perfect score: 7
Sequence: 1 XXXXXXX 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	7	100.0	7	1 ALL2_CARMA	P81805 carcinus ma
2	7	100.0	7	1 ALL3_CARMA	P81806 carcinus ma
3	7	100.0	7	1 ALL4_CARMA	P81807 carcinus ma
4	7	100.0	7	1 ALL5_CARMA	P81808 carcinus ma
5	7	100.0	7	1 ALL7_CYPDO	P82158 cydia pomon
6	7	100.0	7	1 BRHP_CONIM	P58803 conus imper
7	7	100.0	7	1 CARP_MYTED	P10420 mytilus edu
8	7	100.0	7	1 CCF1_ENTFA	P20104 enterococcu
9	7	100.0	7	1 CHOX_ALGSP	P16101 alcaligenes
10	7	100.0	7	1 CIA_ENTFA	P11932 enterococcu
11	7	100.0	7	1 EI05_LITRU	P82101 litoria rub
12	7	100.0	7	1 FAR1_ASCSU	P31889 ascaris suu
13	7	100.0	7	1 FAR1_HELTI	P41871 helisoma tr
14	7	100.0	7	1 FAR1_MACRS	P83274 macrobrachi
15	7	100.0	7	1 FAR1_PROCL	P38499 procambarus
16	7	100.0	7	1 FAR2_ASCSU	P31890 ascaris suu
17	7	100.0	7	1 FAR2_PROCL	P38498 procambarus
18	7	100.0	7	1 FAR3_HAECC	P81298 haemonchus
19	7	100.0	7	1 FAR3_PANRE	P41874 panagrellus
20	7	100.0	7	1 FAR4_PANRE	P41875 panagrellus
21	7	100.0	7	1 FAR5_HIRNE	P42564 hirudo medi
22	7	100.0	7	1 FAR6_CALVO	P41866 calliphora
23	7	100.0	7	1 GRFP_MOUSE	P99025 mus musculu
24	7	100.0	7	1 HY7_FIG	P01153 sus scrofa
25	7	100.0	7	1 IGAO_DACDE	P06294 dactylium d
26	7	100.0	7	1 LANC_CARUI	P36960 carnobacter
27	7	100.0	7	1 MNP1_LEPDE	P42984 leptinotars
28	7	100.0	7	1 PPH2_LYCES	P83379 lycopersico
29	7	100.0	7	1 TFFY_PACDA	P83455 pachymedusa
30	7	100.0	7	1 TY51_LITRU	P82065 litoria rub
31	7	100.0	7	1 UC24_MAIZE	P80630 zea mays (m
32	7	100.0	7	1 UF03_MOUSE	P38641 mus musculu
33	7	100.0	7	1 UF04_MOUSE	P38642 mus musculu

ALIGNMENTS

RESULT 1

ALL2_CARMA
ID ALL2_CARMA STANDARD; PRT; 7 AA.
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 2.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTROPHIC FACTOR OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 7
SQ SEQUENCE 7 AA; 770 MW; 672879CDCBSDB70 CRC64;
Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
Db 1 EAYAFGL 7

RESULT 2

ALL3_CARMA
ID ALL3_CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;

RT "Isolation and identification of multiple neuropeptides of the
 RL allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
 Db 1 EPYAFGL 7

RESULT 3

ALL4_CARMA
 ID ALL4_CARMA STANDARD; PRT; 7 AA.
 AC P81807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 4.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
 Db 1 DPYAFGL 7

RESULT 4

ALL5_CARMA
 ID ALL5_CARMA STANDARD; PRT; 7 AA.
 AC P81808;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 5.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the

RT allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
 Db 1 NPYAFGL 7

RESULT 5

ALL7_CYPDPO
 ID ALL7_CYPDPO STANDARD; PRT; 7 AA.
 AC P82158;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 7.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
 Db 1 KMYDFGL 7

RESULT 6

BRHP_CONIM
 ID BRHP_CONIM STANDARD; PRT; 7 AA.
 AC P58803;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bromheptapeptide Im.
 OS Conus imperialis (Imperial cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=35631;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=97184108; PubMed=9030520;
 RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
 RA McIntosh J.M.;
 RT "A novel post-translational modification involving bromination of

RT tryptophan. Identification of the residue, L-6-bromotryptophan, in
 RT peptides from *Conus imperialis* and *Conus radiatus* venom.";
 RL J. Biol. Chem. 272:4689-4698(1997).
 CC -!- FUNCTION: Does not elicit gross behavioral symptoms when injected
 CC centrally or peripherally in mice.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.
 DR PIR: A58512; A58512.
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.
 FT DISULFID 2 7
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 6 6 BROMINATION.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXXX 7
 Db 1 QCGQAWC 7

RESULT 7

CARP MYTED
 ID CARP MYTED STANDARD; PRT; 7 AA.
 AC P10420;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE Catch-relaxing peptide (CARP).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88052022; PubMed=3676797;
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
 RA Muneoka Y.;
 RT "Catch-relaxing peptide isolated from *Mytilus* pedal ganglia.";
 RL Brain Res. 422:374-376(1987).
 CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
 CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
 CC RETRACTOR MUSCLE.
 DR PIR: A29342; ECMUCR.
 KW Hormone; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXXX 7
 Db 1 AMPMLRL 7

RESULT 8

CCF1 ENTFA
 ID CCF1 ENTFA STANDARD; PRT; 7 AA.
 AC P20104;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CCF10.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=89008313; PubMed=3139658;
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 RA Adsit J.C., Dunny G.M., Suzuki A.;
 RT "Structure of CCF10, a peptide sex pheromone which induces
 RT conjugative transfer of the *Streptococcus faecalis* tetracycline
 RT resistance plasmid, pCF10.";
 RL J. Biol. Chem. 263:14574-14578(1988).
 CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PCF10.
 DR PIR: A30812; A30812.
 KW Pheromone.
 SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXXX 7
 Db 1 LVTLVFV 7

RESULT 9

CHOX ALCSP
 ID CHOX ALCSP STANDARD; PRT; 7 AA.
 AC P16101;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Choline oxidase (EC 1.1.3.17) (Fragment).
 OS Alcaligenes sp.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Alcaligenes.
 OX NCBI_TaxID=512;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81006769; PubMed=6997283;
 RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
 RT "Identification and properties of the prosthetic group of choline
 RT oxidase from *Alcaligenes* sp.";
 RL J. Biochem. 88:197-203(1980).
 CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
 DR PIR: A15398; A15398.
 KW Oxidoreductase.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXXX 7
 Db 1 DNPNSR 7

RESULT 10

CIA ENTFA
 ID CIA ENTFA STANDARD; PRT; 7 AA.
 AC P11332;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87005252; PubMed=3093276;
 RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
 RA White B.A., An F.Y., Clewell D.B., Suzuki A.;

RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
 RT CAM373.";
 RL FEBS Lett. 206:69-72(1986).
 CC -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
 CC HARBORING PAM373.
 CC -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
 CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
 CC -!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
 DR PIR; A25269; A25269.
 KW Pheromone.
 SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
 Db 1 AIFILAS 7

RESULT 11

RT EIO5_LITRU STANDARD; PRT; 7 AA.
 AC P82101;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Electrin 5.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OC NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 7
 FT SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
 Db 1 IYEPEIA 7

RESULT 12

RT FAR1_ASCSU STANDARD; PRT; 7 AA.
 AC P31889;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRamide-like neuropeptide AF1.
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OC NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90180465; PubMed=2627377;
 RA Cowden C., Stretton A.O.W., Davis R.E.;

RT "AF1, a sequenced bioactive neuropeptide isolated from the nematode
 RT Ascaris suum.";
 RL Neuron 2:1465-1473(1989).
 CC -!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTONEURONS. REDUCES THE
 CC INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
 CC CELLS.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 FT SEQUENCE 7 AA; 953 MW; 69D40059CB144350 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
 Db 1 KNEFIRF 7

RESULT 13

RT FAR1_HELTI STANDARD; PRT; 7 AA.
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide GDPFLRF-amide.
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Planorbidae; Helisoma.
 OC NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRamide-related peptides from the kidney of the snail, Helisoma
 RT trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 CC THE KIDNEY, MANTLE AND SKIN.
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7
 FT SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXXXX 7
 Db 1 GDPFLRF 7

RESULT 14

RT FAR1_MACRS STANDARD; PRT; 7 AA.
 AC P83274;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRamide-like neuropeptide FLP1 (DRNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.

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OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigornkul P.; Saraithongkum W., Jaidechoey S., Longyant S.,
RA Sithigornkul W.;
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 DRNFLRF 7

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RESULT 15
FAR1_PROCL
ID FAR1_PROCL STANDARD; PRT; 7 AA.
AC P38499;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cardiac excitatory FMRFamide homolog NF1.
OS Procambarus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Procambarus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183;
RA Mercier A.J.; Orchard I.; Tebrugge V.; Skerrett M.;
RT "Isolation of two FMRFamide-related peptides from crayfish
RT pericardial organs.";
RL Peptides 14:137-143(1993).
CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540A20 CRC64;

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Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
Db 1 NRNFLRF 7

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Search completed: October 28, 2003, 08:58:02
Job time : 25 secs